

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2004, 11:57:59 ; Search time 57.2353 Seconds

(without alignments)
103.669 Million cell updates/sec

Title: US-09-509-449C-5

Perfect score: 123

Sequence: 1 PROSRPSPMGCTDPHRRNRNG 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 645147

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003s:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	21	2	AAW99648 Hepatitis
2	123	100.0	21	3	AAW99648 Hepatitis
3	112	91.1	24	2	AAW99648 Hepatitis
4	112	91.1	25	6	AAW99648 Hepatitis
5	112	91.1	28	2	AAW99648 Hepatitis
6	112	91.1	29	2	AAW99648 Hepatitis
7	111	90.2	20	2	AAW99648 Hepatitis
8	110	89.4	20	2	AAW99648 Hepatitis
9	110	89.4	20	2	AAW99648 Hepatitis
10	105	85.4	20	2	AAW99648 Hepatitis
11	105	85.4	20	2	AAW99648 Hepatitis
12	105	85.4	20	2	AAW99648 Hepatitis
13	105	85.4	20	2	AAW99648 Hepatitis
14	100	81.3	27	2	AAW99648 Hepatitis
15	94	76.4	18	5	AAW99648 Hepatitis
16	94	76.4	19	5	AAW99648 Hepatitis
17	94	76.4	20	2	AAW99648 Hepatitis
18	90	73.2	30	5	AAW99648 Hepatitis
19	85	69.1	15	2	AAW99648 Hepatitis
20	83	67.5	15	4	AAW99648 Hepatitis
21	83	67.5	15	4	AAW99648 Hepatitis
22	83	67.5	15	4	AAW99648 Hepatitis
23	81	65.9	15	4	AAW99648 Hepatitis
24	78	63.4	25	6	AAW99648 Hepatitis
25	67	54.5	15	7	AAW99648 Hepatitis

26	67	54.5	16	4	AAJ03982 Hepatitis
27	67	54.5	20	2	AAW99648 Hepatitis
28	65	52.8	15	7	AAW99648 Hepatitis
29	64	52.0	31	2	AAW99648 Hepatitis
30	62	50.4	15	4	AAW99648 Hepatitis
31	61	49.6	11	4	AAW99648 Hepatitis
32	61	49.6	11	4	AAW99648 Hepatitis
33	57	46.3	18	3	AAW99648 Hepatitis
34	57	46.3	20	2	AAW99648 Hepatitis
35	57	46.3	25	2	AAW99648 Hepatitis
36	56	45.5	20	2	AAW99648 Hepatitis
37	56	45.5	20	2	AAW99648 Hepatitis
38	52	42.3	9	4	AAW99648 Hepatitis
39	52	42.3	9	4	AAW99648 Hepatitis
40	52	42.3	9	4	AAW99648 Hepatitis
41	52	42.3	9	4	AAW99648 Hepatitis
42	52	42.3	9	4	AAW99648 Hepatitis
43	51	41.5	11	4	AAW99648 Hepatitis
44	51	41.5	11	4	AAW99648 Hepatitis
45	51	41.5	11	4	AAW99648 Hepatitis

ALIGNMENTS

RESULT 1
ID AAW99648 standard; peptide; 21 AA.

AC AAW99648;
DT 21-MAY-1999 (first entry)
DE Hepatitis C virus peptide SEQ ID NO:5.

KW Hepatitis C virus; HCV; hepatitis B virus; diagnosis;
KW detection viral infection.
OS Hepatitis C virus.

PN WO9906836-A1.
PD 11-FEB-1999.

PF 04-AUG-1998; 98WO-JP003476.
PR 04-AUG-1997; 97JP-00209515.

PR 04-AUG-1997; 97JP-00209522.
PR 31-UTL-1998; 98UP-00218136.

PA (TOFU) TONEN CORP.

AYagi K, Ohue C, Iida K, Kimura T, Yagi S;
WPI, 1999-153953/13.

PT Detection and assay for, e.g. hepatitis C virus - comprises treatment of
PT the sample with surfactants, protein denaturing agent prior to
PT immunoassay.

PS Example 3; Page 88; 98pp; Japanese.

CC A method has been developed for virus-containing sample is to use a
CC treatment solution comprising: (i) an anionic surfactant; (ii) an
CC amphoteric surfactant; (iii) a non-ionic surfactant; and (iv) a protein
CC denaturing agent. Also described in the present invention are: (1) a
CC similar treatment method by using a solution containing: (i) a chaotropic
CC ion; (ii) an acidifying agent; and (iii) a non-ionic surfactant; (2) an
CC assaying method for viruses by quantitative detection of the presence of
CC viral antigen using a probe for reaction with the specifically recognised
CC viral antigen; (3) a hybridoma cell line chosen from HCl1-11 (FERM BP-
CC 6005), HCl1-14 (FERM BP-6006), HCl1-10 (FERM BP-6004), HCl1-3 (FERM BP-
CC 6002) and HCl1-7 (FERM BP-6003); (4) a monoclonal antibody produced by


```

DE HCV-core derived peptide 1.
XX
XX Hepatitis C virus; HCV; antigen; antibody.
XX
XX Hepatitis C virus.
XX
XX WO2003002749-A2.
XX
XX 09-JAN-2003.
XX
XX 24-JUN-2002; 2002WO-US019958.
XX
XX 26-JUN-2001; 2001US-00891983.
XX
XX 17-JUN-2002; 2002US-00173480.
XX
XX (ABSO ) ABBOTT LAB.
XX
XX Shah DO, Dawson GA, Muerhoff AS, Jiang L, Gutierrez RA, Leary TP,
XX Deal S, Stewart JL;
XX
XX WPI; 2003-201507/19.
XX
XX Detecting hepatitis C virus antigen and antibody in sample, by contacting
XX sample with HCV antigen and antibody, for forming HCV antigen-test
XX antibody complex and HCV antibody-test antigen complex, detecting
XX complexes.
XX
XX Example 1; Page 17; 92pp; English.
XX
XX The invention relates to a novel method for simultaneously detecting a
XX hepatitis C virus (HCV) antigen and an HCV antibody in a test sample. The
XX novel method comprises contacting the test sample with the antigen and
XX antibody, both coated on solid phases, independently, for a time and
XX under conditions sufficient for the formation of an antibody/antigen
XX complex and a second antibody/antigen complex, and detecting the two
XX complexes, which indicate the presence of the antigen and antibody in the
XX test sample. The method is useful for detecting a hepatitis C virus (HCV)
XX antigen and HCV antibody in a test sample. This sequence represents an
XX HCV-core derived peptide relating to the HCV antigen/antibody detection
XX method of the invention
XX
XX Sequence 25 AA;
XX
XX Query Match: 91.1%; Score 112; DB 6; Length 25;
XX Best Local Similarity 90.5%; Pred. No. 1.3e-08;
XX Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 PRGSRPSPGPTDPRRSRNVG 21
XX |||||
XX 5 PRGSRPSPGPTDPRRSRNLG 25
XX
XX RESULT 5
XX AAR33863
XX ID AAR33863 standard; peptide; 28 AA.
XX
XX AAR33863;
XX
XX 25-MAR-2003 (revised)
XX DT 19-JUL-1993 (first entry)
XX
XX Polypeptide p99 comprising HCV viral antigen.
XX
XX Hepatitis C virus; NANBH; assay; antibody; p380-JH1; p380-J; p380LG;
XX p408.
XX
XX Synthetic.
XX
XX WC9306247-A1.
XX
XX 01-APR-1993.
XX
XX 16-SEP-1992; 92WO-US007813.
XX

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XX 16-SEP-1991; 91US-00760292.
PR
XX (ABBO) ABBOTT LAB.
PA
XX Lesniowski RR, Leung TK;
PI
XX WPI; 1993-117563/14.
DR
XX Assay for detecting presence of antibody to hepatitis C viral antigen -
PT by contacting sample with polypeptide coneg. at least one epitope of
PT virus antigen.
XX
XX Disclosure; Page 12; 63pp; English.
PS
XX
XX The synthetic peptide p93 represents amino acid residues 99-126 of the
CC hepatitis C viral antigen. The peptide may be used in an assay to detect
CC antibodies to HCV and thus to diagnose chronic HCV infection. See also
CC AAR33862-87. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 28 AA;
SQ

```

CY      1 PROSRPSPGPTDPRHRNRNGV 21          91.1%; Score 112; DB 2; Length 28;
           |||||||               |       Best Local Similarity 90.5%;
Db      2 PRGSRRPSWGPTDPRRNSRLTG 22         Pred.No.1.4e-08;
                                           Matches   19; Conservative    1; Mismatches     1; Indels        0; Gaps            0

RESULT 6
AAR13347
ID AAR13347 standard; protein; 29 AA.
XX
AC AAR13347;
XX
DT 25-MAR-2003 (revised)
DT 23-OCT-1991 (first entry)
DE P99 HCV antigen (99-126).
XX
KM C100-3; hepatitis C virus; immunosassay; epitope.
XX
OS Synthetic.
PN AU9068390-A.
PD 27-JUN-1991.
XX
PF 21-DEC-1990; 90AU-00068390.
XX
PR 22-DEC-1989; 89US-00456162.
PR 07-NOV-1990; 90US-00610180.
XX
PA (ABSO ) ABBOTT LAB.
PA (LESN/) LESNIEWSKI R.R.
XX
WPI; 1991-238393/33.
XX
PT Immunological assays for hepatitis C virus antibody - by using
PT polypeptide(s) contg. epitope(s) of hepatitis C virus antigens.
XX
PS Claim 10; Page 48; 62pp; English.
CC The polypeptide may be prepared by solid phase synthesis fragment
CC coupling (pret.) or using recombinant technology. The assay has increased
CC sensitivity and is more specific than assays using the polypeptide C100-3
CC (EP-118216). See also AOQ1146-48 and AAR13343-65. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
SQ Sequence 29 AA;
XQ

```

Query Match 91.1%; Score 112; DB 2; Length 29;
 Best Local Similarity 90.5%; Pred. No. 1.5e-08;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RGSRPWGPDPHRSRVNG 21
 |||||
 DB 3 RGSRPWGPDPHRSRVNG 23

RESULT 7

AAR38293
 ID AAR38293 standard; protein; 20 AA.

AC AAR38293;

DT 21-OCT-1993 (first entry)

DE NAMB hepatitis virus HC-OM gene polypeptide CP-5-2.

KW Non-A, non-B; virus; polymerase chain reaction; detection; sensitive;
 KM specific; HCV; NANBH.

OS Non-A.

XX non-B hepatitis virus.

XX JP05091884-A.

XX 16-APR-1993.

XX 10-APR-1991; 91JP-00196175.

XX 12-JUN-1990; 90JP-00153401.

XX 08-NOV-1990; 90JP-00304405.

XX (NAKA/) NAKAMURA T.

XX WPI; 1993-199637/25.

XX N-PSDB; AAQ43903.

XX Antigen related to non-A and non-B hepatitis virus - comprises non-

PT translation region comprising 340 - 341 moles. of nucleotides, non-

PT translation region comprising 1885 - 2551 moles. of nucleotides including

XX region 1,149 and, etc.

XX Claim 29; Page 63; 73pp; Japanese.

XX The sequence is that of NAMB hepatitis virus HC-OM gene polypeptide CP-5-

CC 2. It may be used in a system for detecting NAMB hepatitis. This

CC method is highly specific and sensitive, and can detect NAMB hepatitis

XX virus which could not be detected by conventional methods

XX Sequence 20 AA;

XX Query Match 90.2%; Score 111; DB 2; Length 20;

XX Best Local Similarity 95.0%; Pred. No. 1.4e-08;

XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 2 RGSRPWGPDPHRSRVNG 21

XX 1 RGSRPWGPDPHRSRVNG 20

XX Non-A, non-B; virus; polymerase chain reaction; detection; sensitive;

KW specific; HCV; NANBH.

XX Non-A.

XX non-B hepatitis virus.

XX JP05091884-A.

XX 16-APR-1993.

XX 10-APR-1991; 91JP-00196175.

XX 12-JUN-1990; 90JP-00153401.

XX 08-NOV-1990; 90JP-00304405.

XX (NAKA/) NAKAMURA T.

XX WPI; 1993-199637/25.

XX N-PSDB; AAQ43904.

XX Antigen related to non-A and non-B hepatitis virus - comprises non-

PT translation region comprising 340 - 341 moles. of nucleotides, non-

PT translation region comprising 1885 - 2551 moles. of nucleotides including

XX region 1,149 and, etc.

XX Claim 30; Page 63; 73pp; Japanese.

XX The sequence is that of NAMB hepatitis virus HC-OM gene polypeptide CP-5-

CC 3. It may be used in a system for detecting NAMB hepatitis. This

CC method is highly specific and sensitive, and can detect NAMB hepatitis

XX virus which could not be detected by conventional methods

XX Sequence 20 AA;

XX Query Match 89.4%; Score 110; DB 2; Length 20;

XX Best Local Similarity 90.0%; Pred. No. 2e-08; 0; Indels 0; Gaps 0;

XX Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

XX 2 RGSRPWGPDPHRSRVNG 21

XX 1 RGSRPWGPDPHRSRVNG 20

XX Non-A.

XX non-B hepatitis virus.

XX JP05091884-A.

XX 14-DEC-1994.

XX 27-MAY-1994; 94EP-00108256.

XX 28-MAY-1993; 93JP-00126709.

XX 02-MAR-1994; 94JP-00032201.

XX (EISA) EISAI CO LTD.

XX Aoyama M, Obata T, Tohmatu J, Sawada T, Hosoda T, Iwasaki Y;

PI Arima T;
 XX
 DR WPI; 1995-015655/03.
 XX
 PT New non-A non-B hepatitis virus sub-type - used to develop prods. for
 PT detection, diagnosis, prevention and treatment of non-A non-B hepatitis.
 XX
 PS Example 3; Page 40; 59pp; English.
 XX
 CC AAR67636 is designated M35 and is located at positions 101-120 of the
 CC structural protein (AAR67617) of the Non-A Non-B (NANB) hepatitis virus
 CC encoded by a partial cDNA to genomic RNA sequence. Regions of the
 CC polypeptide were studied for suitability as an epitope. The positive
 CC ratios of the peptide epitope to the plasma of donors, who had been
 CC judged as positive with a reagent of the second generation, i.e., a
 CC second generational anti hepatitis virus antibody detection reagent, were
 CC determined. This peptide had a positive ratio (%) of 31.5. The novel
 CC epitopes are effective in the diagnosis of NANB hepatitis. The nucleotide
 CC sequences (see AAQ75817-19) were isolated from the plasma of donors in
 CC Japan with high s-GTP levels, and were found to be different from
 CC previously reported NANB hepatitis viruses. The DNA can be used as a
 CC reagent for detecting the NANB hepatitis viral gene. The polypeptides can
 CC be used as reagents for detecting anti-NANB hepatitis antibodies or as a
 CC NANB hepatitis viral vaccine. (Updated on 25-MAR-2003 to correct PN
 CC field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 89.4%; Score 110; DB 2; Length 20;
 Best Local Similarity 90.0%; Pred. No. 2e-08;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 2 RGSRRPSWGPTDPRRHSRVNG 21
 |||||:|||||:|||||:
 1 RGSRRPSWGPTDPRRHSRVNG 20
 XX
 RESULT 10
 AAR25132
 ID AAR25132 standard; protein; 20 AA.
 XX
 AC AAR25132;
 XX
 DT 23-DEC-1992 (first entry)
 XX
 DE mock-C3.
 XX
 KM Hepatitis C virus; blood transfusion.
 XX
 OS Synthetic.
 XX
 PN JP04159298-A.
 XX
 PD 02-JUN-1992.
 XX
 PF 19-OCT-1990; 90JP-00282431.
 XX
 PR 19-OCT-1990; 90JP-00282431.
 XX
 PA (OLYU) OLYMPUS OPTICAL CO LTD.
 XX
 WP1; 1992-231947/28.
 XX
 DR New peptides acting as antigenic analogues of human hepatitis C virus -
 DR useful for detecting HCV antibody positive patients.
 PT
 PT
 PS Claim 1; Page 1; 14pp; Japanese.
 XX
 CC The sequences given in AAR25130-35 are peptides which have reactivity to
 CC the antibody against hepatitis C virus (HCV). They can be used on their
 CC own or as a mixture two different peptides. Using these peptides, HCV
 CC antibody positive patients can be detected and hepatitis caused by blood
 CC transfusion can be prevented

XX
 SQ Sequence 20 AA;
 XX
 Query Match 85.4%; Score 105; DB 2; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.9e-08;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 2 RGSRRPSWGPTDPRRHSRVNG 21
 |||||:|||||:|||||:
 1 RGSRRPSWGPTDPRRHSRVNG 20
 XX
 Db 1 RGSRRPSWGPTDPRRHSRVNG 20
 XX
 RESULT 11
 AAR38292
 ID AAR38292 standard; protein; 20 AA.
 XX
 AC AAR38292;
 XX
 DT 21-OCT-1993 (first entry)
 XX
 DE NANB hepatitis virus HC-OM gene polypeptide CP-5-1.
 XX
 KM Non-A, non-B; virus; polymerase chain reaction; detection; sensitive;
 KM specific; HCV; NANBH.
 XX
 OS Non-A.
 OS non-B hepatitis virus.
 XX
 PN JP05091884-A.
 XX
 PD 16-APR-1993.
 XX
 PF 10-APR-1991; 91JP-00196175.
 XX
 PR 12-JUN-1990; 90JP-00153401.
 PR 08-NOV-1990; 90JP-00304405.
 XX
 PA (NAKA/) NAKAMURA T.
 XX
 DR WPI; 1993-199637/25.
 DR N-PSDB; AAQ43902.
 XX
 PT Antigen related to non-A and non-B hepatitis virus - comprises non-
 PT translation region comprising 340 - 341 mols. of nucleotides, non-
 PT translation region comprising 1885 - 2551 mols. of nucleotides including
 PT region 1,149 and, etc.
 XX
 PS Claim 28; Page 63; 73pp; Japanese.
 XX
 CC The sequence is that of NANB hepatitis virus HC-OM gene polypeptide CP-5-
 CC 1. It may be used in a system for detecting NANB hepatitis. This
 CC method is highly specific and sensitive, and can detect NANB hepatitis
 CC virus which could not be detected by conventional methods
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 85.4%; Score 105; DB 2; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.9e-08;
 Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 2 RGSRRPSWGPTDPRRHSRVNG 21
 |||||:|||||:|||||:
 1 RGSRRPSWGPTDPRRHSRVNG 20
 XX
 Db 1 RGSRRPSWGPTDPRRHSRVNG 20
 XX
 RESULT 12
 AAR56608
 ID AAR56608 standard; protein; 20 AA.
 XX
 AC AAR56608;
 XX
 DT 24-MAR-1995 (first entry)
 XX

```

DE HCV peptide NP-11.
XX
XX Hepatitis C virus; HCV; core protein; epitope; T-cell; immunity; CD8;
KM CDB.
XX
XX Hepatitis C virus.
OS
XX JPO6199894-A.
XX
XX 19-JUL-1994.
PD
XX
XX 02-APR-1993; 93JP-00076791.
XX
XX 27-AUG-1992; 92JP-00228965.
XX
XX 10-NOV-1992; 92JP-00299691.
XX
XX (ASAH) ASAH KASEI KOYO KK.
PA (INOM/) INOMAMARI M.
XX
XX WPI; 1994-269451/33.
DR
XX
XX T cell epitope present in the core protein region of Hepatitis C virus
PT (HCV) - used for activation of cellular immunity mechanisms.
XX
XX
XX Disclosure; Fig 2; 14pp; Japanese.
PS
XX
XX A T-cell stimulating peptide is claimed which is ca. 5-20 amino acids
CC long and part of the core protein of HCV and is recognised by and
CC stimulates T-cells. A CD8-positive T-cell stimulating peptide has the
CC sequence given in AAR56606 (NP-9) or AAR56616 (9MA). A CD4-positive T-
CC cell stimulating peptide has the sequence given in AAR56609 (NP-12) or
CC AAR56614 (NP-17). Synthetic peptide mixtures (Mix A: NP-1 - NP-5, Mix B: NP
CC -6 - NP-10, Mix C: NP-11 - NP14, MixD: NP-15 - NP-18) were used in
CC -6 - NP-10, Mix C: NP-11 - NP14, MixD: NP-15 - NP-18) were used in
CC are variants of peptide NP-9
CC
XX
SQ Sequence 20 AA;

Query Match 85.4%; Score 105; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.9e-08;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RGRSRPSWGPDPDRSRNRVNG 21
DB 1 RGRSRPSWGPDPDRSRNRVNG 20

RESULT 13
AAU84604
ID AAU84604 standard; peptide; 30 AA.
XX
XX AAU84604;
AC
XX
XX 08-MAY-2002 (first entry)
DT
XX
XX HCV HepC1a segment 7.
DE
XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX viral infection; human immunodeficiency virus; melanoma;
XX bacterial infection; Salmonella; Legionella; parasitic infection;
XX Trypanosoma; Toxoplasma; Giardia.
XX
XX Hepatitis C virus.
OS
XX
XX WO200190197-A1.
XX
XX 29-NOV-2001.
PD
XX
XX 25-MAY-2001; 2001WO-AU000622.
XX
XX 26-MAY-2000; 2000AU-00007761.
XX
XX (AUSU) UNIV AUSTRALIAN NAT.
PA

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XX
XX Thomson SA, Ramehaw IA;
PI
XX
XX WPI; 2002-147575/19.
DR
XX
XX N-P8DB; ABR36442.
DR
XX
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX
XX Example 2; Fig 26; 364pp; English.
PS
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
CC
XX
SQ Sequence 30 AA;

Query Match 85.4%; Score 105; DB 5; Length 30;
Best Local Similarity 94.7%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRGRSRPSWGPDPDRSRNRN 19
DB 12 PRGRSRPSWGPDPDRSRNRN 30

RESULT 14
AAR31922
ID AAR31922 standard; peptide; 27 AA.
XX
XX AAR31922;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX
XX 03-MAR-1993 (first entry)
DT
XX
XX HCV peptide BCH-443.
DE
XX
XX Hepatitis C virus; vaccine; screening; diagnosis.
XX
XX Synthetic.
OS
XX
XX EP507615-A1.
XX
XX 07-OCT-1992.
PD
XX
XX 03-APR-1992; 92EP-00302975.
XX
XX 05-APR-1991; 91US-00681701.
XX
XX (BIOC-) BIOCHEM PHARMA INC.
PA

```

PI Lacroix M;
 XX
 DR WPI; 1992-333826/41.
 XX
 PT Hepatitis C virus peptide(s) and their mixts. - used for diagnosing and
 PT vaccinating against hepatitis C virus infections.
 XX
 PS Claim 1; Page 27; 34pp; English.
 XX
 CC The peptide BCH-443 was synthesised based upon amino acids 101-127 of
 CC hepatitis C virus (HCV) envelope protein. It is useful as an active
 CC ingredient in vaccines against HCV and can be used for screening and
 CC diagnosing HCV infection. See also AAR31917-R31926. (Updated on 25-MAR-
 CC 2003 to correct FN field.)
 CC
 SQ Sequence 27 AA;
 QY
 Best Match 81.3%; Score 100; DB 2; Length 27;
 Best Local Similarity 85.0%; Pred. No. 6.6e-07;
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Db 1 RGSPPSWGPTDPRRRSRNIG 20

RESULT 15
 AAM50830
 ID AAM50830 standard; peptide; 18 AA.
 AC AAM50830;
 XX
 DT 07-AUG-2003 (revised)
 DT 01-MAY-2002 (first entry)
 XX
 DE HCV core region peptide MDL-8 (aa103-120).
 XX
 KW HCV; MDL-8; infection; diagnosis; vaccine.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200204484-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001; 2001WO-CA000988.
 XX
 PR 07-JUL-2000; 2000CA-02311022.
 XX
 PA (MEDM-) MEDMIRA INC.
 XX
 PI Chan HKW, Theolis R;
 XX
 DR WPI; 2002-179696/23.
 XX
 PT New hepatitis C virus (HCV) peptides and mosaic antigen composition
 PT comprising the peptides, useful as immunoreagents for detecting HCV
 PT antibodies infection, or as an immunogen for stimulating production of
 PT antibodies against HCV.
 XX
 PS Example 1; Page 33; 59pp; English.
 XX
 CC The present sequence is that of peptide MDL-8 comprising amino acid
 CC residues 103-120 of the hepatitis C virus (HCV) polyprotein core region
 CC (see AAM50816). A panel of overlapping peptides between positions 1 and
 CC 186 of the HCV core region was synthesised and tested for
 CC immunoreactivity with a commercially available human serum panel. All of
 CC the immunoreactivity was concentrated within the core region between
 CC amino acids 1 to 80. MDL-8 did not include a major immunodominant region.
 CC The invention provides a highly immunoreactive mosaic antigen composition
 CC (MAC) comprising 2 or more immunoreactive peptides (see AAM50816-27),
 CC each of which is immobilised to a carrier. The unique combination of HCV
 CC core peptides in the MAC provides higher specificity and sensitivity for

CC detection of human antibodies specificity to HCV in rapid HCV diagnostic
 CC applications. An in vitro diagnostic method for detecting anti-HCV
 CC antibodies in a test sample and a diagnostic test kit are provided which
 CC use the MAC as an immunoreagent. The HCV MAC may also potentially be used
 CC as an immunogen in vaccine compositions. (Updated on 07-AUG-2003 to
 CC correct OS field.)
 CC
 SQ Sequence 18 AA;
 QY
 Best Match 76.4%; Score 94; DB 5; Length 18;
 Best Local Similarity 88.9%; Pred. No. 3.1e-06;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 SRPSWGPTDPRRRSRNIG 18

Search completed: June 29, 2004, 12:05:56
 Job time : 58.2353 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2004, 12:03:34 ; Search time 17.2941 Seconds
(without alignments)
62.669 Million cell updates/sec

Title: US-09-509-449C-5
Perfect score: 123
Sequence: 1 PRGSRPSWGPTDPRHRSRVNG 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 227376

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCtus_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	21	US-10-133-007-5	Sequence 5, Appl1
2	112	91.1	24	PCT-US92-07865-15	Sequence 15, Appl1
3	112	91.1	28	US-08-905-054B-3	Sequence 3, Appl1
4	112	91.1	28	PCT-US92-07813-3	Sequence 3, Appl1
5	100	81.3	27	US-07-681-701-10	Sequence 10, Appl1
6	94	76.4	20	US-08-635-886C-8	Sequence 8, Appl1
7	94	76.4	20	US-08-974-690C-8	Sequence 8, Appl1
8	85	69.1	15	US-08-604-565-22	Sequence 22, Appl1
9	85	69.1	15	US-09-689-678-22	Sequence 22, Appl1
10	64	52.0	31	US-08-473-475A-25	Sequence 25, Appl1
11	57	46.3	20	US-08-635-886C-9	Sequence 9, Appl1
12	57	46.3	20	US-08-974-690C-9	Sequence 9, Appl1
13	56	45.5	20	US-10-133-007-6	Sequence 6, Appl1
14	50	40.7	8	US-08-444-818-301	Sequence 301, Appl1
15	49	39.8	8	US-08-444-818-299	Sequence 299, Appl1
16	49	39.8	8	US-08-444-818-302	Sequence 302, Appl1
17	48	39.0	8	US-08-444-818-300	Sequence 300, Appl1
18	44	35.8	29	US-09-205-258-330	Sequence 630, Appl1
19	43	35.0	31	US-09-368-045A-31	Sequence 31, Appl1
20	40.5	32.9	35	US-09-368-009-28	Sequence 28, Appl1
21	40.5	32.9	35	US-08-809-156B-28	Sequence 28, Appl1
22	39.5	32.1	40	US-09-314-868-106	Sequence 106, Appl1
23	39	31.7	40	US-09-071-824-36	Sequence 36, Appl1
24	38.5	31.3	40	US-09-314-868-107	Sequence 107, Appl1
25	38	30.9	8	US-08-444-818-298	Sequence 298, Appl1
26	38	30.9	31	US-09-308-345A-34	Sequence 34, Appl1
27	38	30.9	39	US-08-390-353A-11	Sequence 11, Appl1

28	38	30.9	39	4	US-09-101-059-11	Sequence 11, Appl1
29	37	30.1	31	4	US-09-308-345A-32	Sequence 32, Appl1
30	37	30.1	31	4	US-09-308-345A-33	Sequence 33, Appl1
31	36	29.3	16	2	US-08-676-279-6	Sequence 6, Appl1
32	36	29.3	17	2	US-08-676-279-12	Sequence 12, Appl1
33	36	29.3	17	4	US-08-951-034B-14	Sequence 14, Appl1
34	36	29.3	20	4	US-08-635-886C-54	Sequence 54, Appl1
35	36	29.3	20	4	US-08-974-690C-54	Sequence 47, Appl1
36	35.5	28.9	24	1	US-08-244-701B-47	Sequence 47, Appl1
37	35.5	28.9	24	4	US-09-076-721-47	Sequence 47, Appl1
38	35.5	28.9	33	4	US-08-469-260A-306	Sequence 306, Appl1
39	35.5	28.9	33	4	US-08-488-446-306	Sequence 306, Appl1
40	35.5	28.9	33	4	US-08-467-344A-306	Sequence 306, Appl1
41	35	28.5	21	3	US-09-184-658-68	Sequence 68, Appl1
42	35	28.5	21	4	US-09-504-262D-68	Sequence 68, Appl1
43	35	28.5	37	4	US-09-314-268-109	Sequence 109, Appl1
44	34	27.6	7	1	US-08-460-343B-6	Sequence 6, Appl1
45	34	27.6	7	1	US-08-398-028B-6	Sequence 6, Appl1

ALIGNMENTS

```
RESULT 1
US-10-133-007-5
; Sequence 5, Application US/10133007
; Patent No. 6623921
; GENERAL INFORMATION:
; APPLICANT: Aoyagi, Katsumi
; APPLICANT: Ohue, Chiharu
; APPLICANT: Iida, Kuniko
; APPLICANT: Yagi, Shinaro
; TITLE OF INVENTION: METHOD FOR MEASUREMENT OF HEPATITIS C VIRUS
; FILE REFERENCE: 594.352USWO
; CURRENT APPLICATION NUMBER: US/10/133,007
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US/09/509,449
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: JP 10-216094
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/JP99/04129
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
US-10-133-007-5

Query Match          100.0%; Score 123; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPTDPRHRSRVNG 21
Db 1 PRGSRPSWGPTDPRHRSRVNG 21

RESULT 2
PCT-US92-07865-15
; Sequence 15, Application PC/TUS9207865
; GENERAL INFORMATION:
; APPLICANT: Dreesman, Jordan R.
; APPLICANT: Burk, Kenneth H.
; APPLICANT: Pauletti, Daniel
; TITLE OF INVENTION: Peptide-based Hepatitis C Virus
; TITLE OF INVENTION: Immunoassays
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
```

STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07865
FILING DATE: 19920916
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 16-SEP-1991
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Rabian, Gary R. 33,875
REGISTRATION NUMBER: 1600-0086.41
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Hepatitis C Virus
INDIVIDUAL ISOLATE: Dp10, amino acids 98-121 of the HCV
INDIVIDUAL ISOLATE: polypotein
PCT-US92-07865-15

Query Match 91.1%; Score 112; DB 5; Length 24;
Best Local Similarity 90.5%; Pred. No. 1.1e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPDPHRRSRNVG 21
|||||
Db 3 PRGSRPSWGPDPHRRSRNVG 23

RESULT 3
US-08-905-054B-3
Sequence 3, Application US/08905054B
Patent No. 6596476
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Lesniowski, Richard R.
APPLICANT: Leung, Tat K.
TITLE OF INVENTION: HEPATITIS C ASSAY
FILE REFERENCE: 4767.US.C7
CURRENT APPLICATION NUMBER: US/08/905.054B
CURRENT FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/707,355
PRIOR FILING DATE: 1996-09-04
PRIOR APPLICATION NUMBER: US 08/507,740
PRIOR FILING DATE: 1995-07-26
PRIOR APPLICATION NUMBER: US 08/373,920
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: US 08/183,207
PRIOR FILING DATE: 1994-01-18
PRIOR APPLICATION NUMBER: US 07/760,292
PRIOR FILING DATE: 1991-09-16
PRIOR APPLICATION NUMBER: US 07/610,180
PRIOR FILING DATE: 1990-11-07
PRIOR APPLICATION NUMBER: US 07/456,162

PRIOR FILING DATE: 1989-12-22
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 28
TYPE: PRT
ORGANISM: Hepatitis C Virus
US-08-905-054B-3

Query Match 91.1%; Score 112; DB 4; Length 28;
Best Local Similarity 90.5%; Pred. No. 1.3e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPDPHRRSRNVG 21
|||||
Db 2 PRGSRPSWGPDPHRRSRNVG 22

RESULT 4
PCT-US92-07813-3
Sequence 3, Application PC/TUS9207813
GENERAL INFORMATION:
APPLICANT: LESNIEWSKI, RICHARD R.
APPLICANT: LEUNG, TAT K.
TITLE OF INVENTION: HEPATITIS C ASSAY
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: ABBOTT LABORATORIES CHAD377/APED
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07813
FILING DATE: 19920916
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKIP, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4767.P3.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-07813-3

Query Match 91.1%; Score 112; DB 5; Length 28;
Best Local Similarity 90.5%; Pred. No. 1.3e-09;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPDPHRRSRNVG 21
|||||
Db 2 PRGSRPSWGPDPHRRSRNVG 22

RESULT 5
US-07-681-701-10
Sequence 10, Application US/07681701
Patent No. 5574132
GENERAL INFORMATION:
APPLICANT: Lacroix, Martial

```

; TITLE OF INVENTION: PEPTIDES AND MIXTURES THEREOF FOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/681,701
; FILING DATE: 19910405
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: IAF-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 715-0742
; TELEFAX: (212) 715-0673
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-681-701-10

Query Match      81.3%; Score 100; DB 1; Length 27;
Best Local Similarity 85.0%; Pred. No. 6.7e-08;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 RGSRRPSWGPTDPRRRSNNV 21
Db      1 RGSRRPSWGPTDPRRRSNNV 20

RESULT 6
US-08-635-886C-8
; Sequence 8, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
;
US-08-635-886C-8

Query Match      76.4%; Score 94; DB 4; Length 20;
Best Local Similarity 94.1%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 PRGSRPSWGPTDPRRRS 17
Db      4 PRGSRPSWGPTDPRRRS 20

RESULT 7
US-08-974-690C-8
; Sequence 8, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
;
US-08-974-690C-8

Query Match      76.4%; Score 94; DB 4; Length 20;
Best Local Similarity 94.1%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 PRGSRPSWGPTDPRRRS 17
Db      4 PRGSRPSWGPTDPRRRS 20

RESULT 8
US-08-604-365-22
; Sequence 22, Application US/08604365
; Patent No. 6183949
; GENERAL INFORMATION:
; APPLICANT: Seidel, Christoph; Erlich-Weinreich,
; APPLICANT: Gertraud, Bayer, Hubert; Wiennues, Ursula; Jung,
; APPLICANT: Gntner-Gernard, Inlefeldt, Hans Georg
; TITLE OF INVENTION: HCV Peptide Antigens and Methods for
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,365
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,398
; FILING DATE: 11-MARCH-1993
; APPLICATION NUMBER: PCT/EP92/01468
; FILING DATE: 30-JUNE-1992
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: DE 41 22 160.5
FILING DATE: 04-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 41 41 304.0
FILING DATE: 14-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 42 09 216.9
FILING DATE: 21-MARCH-1992
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: BOER 1010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-604-365-22

Query Match 69.1%; Score 85; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPTDPR 14
DB 1 PRGSRPSWGPTDPR 14

RESULT 9
US-09-689-678-22
Sequence 22, Application US/09689678
Patent No. 6592871
GENERAL INFORMATION:
APPLICANT: Seidel, Christoph, Ehrlich-Weinreich,
Gertraud; Bayer, Hubert; Wienhues, Ursula; Jung,
Gunter-Gerhard; Ihlenfeldt, Hans Georg
TITLE OF INVENTION: HCV Peptide Antigens and Methods for
the Determination of HCV
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,678
FILING DATE: 13-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/604,365
FILING DATE: <Unknown>
APPLICATION NUMBER: 07/977,398
FILING DATE: 11-MARCH-1993
APPLICATION NUMBER: PCT/EP92/01468
FILING DATE: 30-JUNE-1992
APPLICATION NUMBER: DE 41 22 160.5
FILING DATE: 04-JULY-1991
APPLICATION NUMBER: DE 41 41 304.0
FILING DATE: 14-DEC-1991
APPLICATION NUMBER: DE 42 09 216.9
FILING DATE: 21-MARCH-1992
ATTORNEY/AGENT INFORMATION:

NAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: BOER 1010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-689-678-22

Query Match 69.1%; Score 85; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPTDPR 14
DB 1 PRGSRPSWGPTDPR 14

RESULT 10
US-08-473-475A-25
Sequence 25, Application US/08473475A
Patent No. 5843450
GENERAL INFORMATION:
APPLICANT: DAMSON, GEORGE
APPLICANT: BRIDON, DOMINIQUE P.
APPLICANT: SCHROEDER-POLIAK, PAMELLA A.
APPLICANT: KNIGGE, MARK F.
APPLICANT: JAFFE, KEEVE
TITLE OF INVENTION: HEPATITIS GB VIRUS SYNTHETIC PEPTIDES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,475A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33206
REFERENCE/DOCKET NUMBER: 5527US.P8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-2623
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-475A-25

Query Match 52.0%; Score 64; DB 2; Length 31;
Best Local Similarity 71.4%; Pred. No. 0.011;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 WGPDPHRSRNVG 21
Db 4 WGRDPHRSRNLG 17

RESULT 11
US-08-635-886C-9
; Sequence 9, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635, 886C
; PRIOR FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-9

Query Match 46.3%; Score 57; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.07;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 10 PTPDRHRSRNVG 21
Db 1 PTPDRHRSRNLG 12

RESULT 12
US-08-974-690C-9
; Sequence 9, Application US/08974690C
; Patent No. 661333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974, 690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-9

Query Match 46.3%; Score 57; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.07;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 10 PTPDRHRSRNVG 21
Db 1 PTPDRHRSRNLG 12

RESULT 13
US-10-133-007-6
; Sequence 6, Application US/10133007
; Patent No. 6623921
; GENERAL INFORMATION:
; APPLICANT: Aoyagi, Katsumi
; APPLICANT: Ohue, Chiharu
; APPLICANT: Iida, Kumiko
; APPLICANT: Yagi, Shintaro
; TITLE OF INVENTION: METHOD FOR MEASUREMENT OF HEPATITIS C VIRUS
; FILE REFERENCE: 594.352USMO
; CURRENT APPLICATION NUMBER: US/10/133, 007
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US/09/509, 449
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: JP 10-216094
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/JP99/04129
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fused polypeptide including Hepatitis C virus sequence.
US-10-133-007-6

Query Match 45.5%; Score 56; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 DPHRSRNVG 21
Db 1 DPHRSRNVG 10

RESULT 14
US-08-444-818-301
; Sequence 301, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Rutter, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444, 818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403, 590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardin, Aissa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885

; INFORMATION FOR SEQ ID NO: 301:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-444-818-301

Query Match 40.7%; Score 50; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSRPSWGP 10
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 1 GSRPSWGP 8

RESULT 15
 US-08-444-818-299
 ; Sequence 299, Application US/08444818
 ; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rulter, William J.
 ; TITLE OF INVENTION: NANBY Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hardin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110,002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 299:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-444-818-299

Query Match 39.8%; Score 49; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGSRPSW 8
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 1 PRGSRPSW 8

Search completed: June 29, 2004, 12:09:59
 Job time: 17.2941 secs

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OM protein - protein search, using sw model

Run on: June 29, 2004, 12:08:25 ; Search time 43.2353 Seconds

(without alignments)
137.314 Million cell updates/sec

Title: US-09-509-449C-5
Perfect score: 123
Sequence: 1 PRGSRPWCPTDPRHRRNNG 21

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

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Maximum DB seq length: 40

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Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

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- 14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	91.1	25	10	US-09-891-983A-29
2	112	91.1	25	14	US-10-173-480-56
3	105	85.4	30	12	US-10-296-734-420
4	94	76.4	20	12	US-10-651-165-8
5	90	73.2	30	12	US-10-296-734-422
6	85	63.1	15	14	US-10-371-540-22
7	78	63.4	25	10	US-09-891-983A-30
8	78	63.4	25	14	US-10-173-480-57
9	67	54.5	15	14	US-10-268-569-11
10	67	54.5	15	14	US-10-268-569-11
11	65	52.8	15	14	US-10-268-569-12
12	65	52.8	15	14	US-10-268-569-12
13	57	46.3	20	12	US-10-651-165-9
14	54	43.9	18	15	US-10-350-719-180
15	49	39.8	9	8	US-08-344-824-83

16	49	39.8	17	10	US-09-891-983A-28	Sequence 28, App1
17	49	39.8	17	14	US-10-173-480-55	Sequence 55, App1
18	44.5	36.2	35	14	US-10-029-386-33805	Sequence 33805, A
19	44	35.8	29	10	US-09-933-767-630	Sequence 630, App
20	44	35.8	29	12	US-10-004-860-630	Sequence 630, App
21	44	35.8	29	14	US-10-023-282-530	Sequence 630, App
22	44	35.8	31	14	US-10-029-386-28430	Sequence 28430, A
23	42	34.1	38	9	US-09-836-392-30	Sequence 30, App1
24	40.5	32.9	35	10	US-09-775-964-28	Sequence 28, App1
25	40.5	32.9	39	9	US-09-925-302-681	Sequence 681, App
26	40.5	32.9	39	12	US-09-925-302-681	Sequence 681, App
27	40	32.5	10	14	US-10-228-806-61	Sequence 61, App1
28	40	32.5	10	15	US-10-100-303A-48	Sequence 48, App1
29	40	32.5	31	14	US-10-144-929-252	Sequence 252, App
30	39.5	32.1	37	15	US-10-144-929-252	Sequence 252, App
31	39.5	32.1	37	14	US-10-029-386-31465	Sequence 31465, A
32	39.5	32.1	40	14	US-10-008-524A-106	Sequence 106, App
33	39.5	32.1	40	15	US-10-350-719-106	Sequence 106, App
34	39	31.7	9	8	US-08-344-824-84	Sequence 84, App1
35	39	31.7	9	16	US-10-440-330-29	Sequence 29, App1
36	39	31.7	24	14	US-10-194-441A-83	Sequence 83, App1
37	39	31.7	31	9	US-09-880-578-36	Sequence 36, App1
38	38.5	31.3	35	9	US-09-864-764-37459	Sequence 37459, A
39	38.5	31.3	40	14	US-10-008-524A-107	Sequence 107, App
40	38.5	31.3	40	15	US-10-350-719-107	Sequence 107, App
41	38	30.9	21	14	US-10-084-813-347	Sequence 347, App
42	38	30.9	21	14	US-10-084-813-348	Sequence 348, App
43	38	30.9	21	14	US-10-084-813-349	Sequence 349, App
44	38	30.9	28	10	US-09-974-879-564	Sequence 564, App
45	38	30.9	28	10	US-09-305-736-569	Sequence 569, App

ALIGNMENTS

RESULT 1
US-09-891-983A-29
Sequence 29, Application US/09891983A
Publication No. US20030108858A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Shah, Dinesh O.
APPLICANT: Dawson, George A.
APPLICANT: Muirhoff, A. Scott
APPLICANT: Jiang, Lily
APPLICANT: Gutierrez, Robin A.
APPLICANT: Leary, Thomas P.
APPLICANT: Dealy, Suresh
APPLICANT: Stewart, James L.
TITLE OF INVENTION: Methods For The simultaneous Detection
FILE REFERENCE: 6821 US 01
CURRENT APPLICATION NUMBER: US/09/891, 983A
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 29
LENGTH: 25
TYPE: PRT
ORGANISM: Hepatitis C Virus
US-09-891-983A-29

Query Match 91.1%, Score 112, DB 10, Length 25;
Best Local Similarity 90.5%, Pred. No. 1.7e-07;
Matches 19, Conservative 1, Mismatches 1, Gaps 0;

QY 1 PRGSRPWCPTDPRHRRNNG 21
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DB 5 PRGSRPWCPTDPRHRRNNG 25

RESULT 2
US-10-173-480-56

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; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELBEYS, Robert
; APPLICANT: MARTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-8

Query Match
Best Local Similarity 76.4%; Score 94; DB 12; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 PRGSRPSMGPTDRHRS 17
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Db 4 PRGSRPSMGPTDRHRS 20

RESULT 5
US-10-296-734-422
; Sequence 422, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 422
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HepC 1a segment 8
US-10-296-734-422

Query Match
Best Local Similarity 73.2%; Score 90; DB 12; Length 30;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 5 RPSMGPTDRHRSRVNG 21
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Db 1 RPSMGPTDRHRSRVNG 17

RESULT 6
US-10-371-540-22
; Sequence 22, Application US/10371540
; Publication No. US20030198644A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: HCV PEPTIDE ANTIGENS AND METHODS FOR THE DETERMINATION OF HCV
; FILE REFERENCE: 9793/129

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; CURRENT APPLICATION NUMBER: US/10/371,540
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 09/689,678
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 08/604,365
; PRIOR FILING DATE: 1996-02-21
; PRIOR APPLICATION NUMBER: P 41 41 304.1
; PRIOR FILING DATE: 1991-12-14
; PRIOR APPLICATION NUMBER: P 42 09 215.9
; PRIOR FILING DATE: 1992-03-21
; PRIOR APPLICATION NUMBER: PCT/EP92/01468
; PRIOR FILING DATE: 1992-06-30
; PRIOR APPLICATION NUMBER: P 41 22 160.5
; PRIOR FILING DATE: 1991-07-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent version 3.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide antigen for anti-HCV antibodies
US-10-371-540-22

Query Match          69.1%; Score 85; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPTDPR 14
Db 1 PRGSRPSWGPTDPR 14

RESULT 7
US-09-891-983A-30
; Sequence 30, Application US/09891983A
; Publication No. US20030108858A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Shah, Dinesh O.
; APPLICANT: Dawson, George A.
; APPLICANT: Muerhoff, A. Scott
; APPLICANT: Jiang, Lily
; APPLICANT: Gutierrez, Robin A.
; APPLICANT: Leary, Thomas P.
; APPLICANT: Desai, Suresh
; APPLICANT: Stewart, James L.
; TITLE OF INVENTION: Methods For The simultaneous Detection
; FILE REFERENCE: 6821.US.01
; CURRENT APPLICATION NUMBER: US/09/891,983A
; CURRENT FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-09-891-983A-30

Query Match          63.4%; Score 78; DB 10; Length 25;
Best Local Similarity 86.7%; Pred. No. 0.0038;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 SWGPTDPRRRSRNG 21
Db 1 SWGPTDPRRRSRNG 15

RESULT 8
US-10-173-480-57
; Sequence 57, Application US/10173480
; Publication No. US20030152948A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Shah, Dinesh O.
; APPLICANT: Dawson, George A.
; APPLICANT: Muerhoff, A. Scott
; APPLICANT: Jiang, Lily
; APPLICANT: Gutierrez, Robin A.
; APPLICANT: Leary, Thomas P.
; APPLICANT: Desai, Suresh
; APPLICANT: Stewart, James L.
; TITLE OF INVENTION: METHODS FOR THE SIMULTANEOUS DETECTION
; FILE REFERENCE: 6821.US.P1
; CURRENT APPLICATION NUMBER: US/10/173,480
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/891,983
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV-Core derived peptides
US-10-173-480-57

Query Match          63.4%; Score 78; DB 14; Length 25;
Best Local Similarity 86.7%; Pred. No. 0.0038;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 SWGPTDPRRRSRNG 21
Db 1 SWGPTDPRRRSRNG 15

RESULT 9
US-10-268-561-11
; Sequence 11, Application US/10268561
; Publication No. US20030148333A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: HCV Anti-Core Monoclonal Antibodies
; FILE REFERENCE: CDS0286
; CURRENT APPLICATION NUMBER: US/10/268,561
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/337453
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-268-561-11

Query Match          54.5%; Score 67; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPT 11
Db 5 PRGSRPSWGPT 15

RESULT 10
US-10-268-569-11
; Sequence 11, Application US/10268569
; Publication No. US20030152965A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: HCV Core Protein Sequences
; FILE REFERENCE: CDS-0286
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CURRENT APPLICATION NUMBER: US/10/268,569
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/347,303
; PRIOR FILING DATE: 2001-11-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-268-569-11

Query Match 54.5%; Score 67; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPT 11
DB 5 PRGSRPSWGPT 15

RESULT 11
US-10-268-561-12
; Sequence 12, Application US/10268561
; Publication No. US2003014833A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: HCV Anti-Core Monoclonal Antibodies
; FILE REFERENCE: CDS0286
; CURRENT APPLICATION NUMBER: US/10/268,561
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/337453
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-268-561-12

Query Match 52.8%; Score 65; DB 14; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SWGPTDPRHRSR 18
DB 1 SWGPTDPRHRSR 12

RESULT 12
US-10-268-569-12
; Sequence 12, Application US/10268569
; Publication No. US20030152965A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: HCV Core Protein Sequences
; FILE REFERENCE: CDS-0288
; CURRENT APPLICATION NUMBER: US/10/268,569
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/347,303
; PRIOR FILING DATE: 2001-11-11
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-268-569-12

Query Match 52.8%; Score 65; DB 14; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.11;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SWGPTDPRHRSR 18
DB 1 SWGPTDPRHRSR 12

RESULT 13
US-10-651-165-9
; Sequence 9, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELBYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; PRIOR FILING DATE: 2003-09-02
; CURRENT APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-9

Query Match 46.3%; Score 57; DB 12; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 PTDPRHRSRNVG 21
DB 1 PTDPRHRSRNVG 12

RESULT 14
US-10-350-719-180
; Sequence 180, Application US/10350719
; Publication No. US20030219726A1
; GENERAL INFORMATION:
; APPLICANT: Dootbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
; TITLE OF INVENTION: VIRUSES
; FILE REFERENCE: 18396/2162
; CURRENT APPLICATION NUMBER: US/10/350,719
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/GB01/01176
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: GB0018140.4
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 180
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human papillomavirus type 51
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)-(18)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-350-719-180

Query Match 43.9%; Score 54; DB 15; Length 18;
Best Local Similarity 57.1%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Wed Jun 30 11:14:03 2004

us-09-509-449c-5.rapb

Page 5

Qy 6 PSMGPTDPRHRSRN 19
Db 3 PAMAPKPKPRHNSN 16

RESULT 15
US-08-344-824-83
; Sequence 83, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alesandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-344-824-83

Query Match 39.8%; Score 49; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 1 PRGSRPSW 8
Db 2 PRGSRPSW 9

Search completed: June 29, 2004, 12:21:22
JOB time : 44.2353 secs

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OM protein - protein search, using sw model

Run on: June 29, 2004, 12:02:29 ; Search time 14 Seconds

(without alignments)
144.287 Million cell updates/sec

Title: US-09-509-449C-5

Sequence: 1 PRGSRPSWGPDPHRSRNVG 21

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 9205

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum March 0%
Maximum March 100%

Listing first 45 summaries

Database : PIR 78: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	30.9	23	2	S10448	nucleocapsid prote
2	37.5	30.5	29	2	C40638	orf 3' of cycl - R
3	34	27.6	37	2	B70566	probable ribosomal
4	33.5	27.2	24	2	S43011	merp protein - Yer
5	33	26.8	28	2	S51593	myrb protein - Mic
6	33	26.8	33	1	IRTR1A	protamine IA - rat
7	33	26.8	37	2	D87154	50S ribosomal prot
8	32.5	26.4	29	2	T34643	hypothetical prote
9	32	26.0	38	2	S17889	ribosomal protein
10	32	26.0	38	2	D95027	ribosomal protein
11	32	26.0	38	2	D97898	50S ribosomal prot
12	32	26.0	38	2	S58601	hypothetical prote
13	31	25.2	33	2	C21211	protamine TP16 - r
14	31	25.2	33	2	E21211	protamine TP21 - r
15	31	25.2	33	2	A42592	phycocyanin-6x reduc
16	31	25.2	38	2	G45095	photosystem I 11gh
17	31	25.2	39	2	S71186	DNA-directed RNA p
18	30	24.4	11	2	S70338	naph small chain
19	30	24.4	32	1	BSPGNB	neuremedin B-32 -
20	30	24.4	38	2	D84988	50S ribosomal prot
21	30	24.4	40	2	A42087	liopopeptide mating
22	29	23.6	27	2	C44908	chitinase (EC 3.2.
23	29	23.6	28	2	A50692	proline-rich prote
24	29	23.6	31	2	S14615	hypothetical prote
25	29	23.6	32	1	S10NA1	protamine A1 - chu
26	29	23.6	33	1	IRTR59	protamine CII - ra
27	29	23.6	33	1	IRTR42	protamine 2c - rat
28	29	23.6	33	2	A21211	protamine TP14 - r
29	23.6	23	2	2	D21211	protamine TP17 - r

30	29	23.6	33	2	S00710	protamine CII - ch
31	29	23.6	33	2	T01070	protamine - raibo
32	29	23.6	34	2	A24174	thermomycollin (EC
33	29	23.6	35	2	JN0369	microbial serine p
34	29	23.6	37	1	R5NT36	ribosomal protein
35	29	23.6	37	2	S78391	ribosomal protein
36	29	23.6	38	2	H83113	50S ribosomal prot
37	29	23.6	39	2	C97513	hypothetical prote
38	28.5	23.2	36	2	G87666	hypothetical prote
39	28	22.8	10	2	S53789	neuropeptide Pec-H
40	28	22.8	20	2	PC2084	serine proteinase
41	28	22.8	20	2	S23981	outer layer protei
42	28	22.8	27	2	A28391	hypothetical prote
43	28	22.8	29	2	S08555	ribosomal protein
44	28	22.8	30	2	S14062	hypothetical prote
45	28	22.8	30	2	E45095	photosystem I 11gh

ALIGNMENTS

RESULT 1
S10448
nucleocapsid protein - porcine transmissible gastroenteritis virus (fragment)
C/Species: porcine transmissible gastroenteritis virus
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 20-Sep-1999
C/Accession: S10448
R/Page, K.W.; Britton, P.; Boulton, M.E.G.
submitted to the EMBL Data Library, March 1990
A/Reference number: S10447
A/Accession: S10448
A/Molecule type: mRNA
A/Residues: 1-23 <PAG>
A/Cross-references: EMBL:X52157; NID:G59010; PIDN:CAA36410.1; PID:G59011
C/Suprafamily: coronavirus nucleocapsid protein
C/Keywords: nucleocapsid

Query Match 30.9%; Score 39; DB 2; Length 23;
Best Local Similarity 38.9%; Pred. No. 46;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 RGRSPSWGPDPHRSRV 19
DB 4 QGQVSWGDESTKIRGRS 21

RESULT 2
C40638
orf 3' of cycl - Rhodobacter sphaeroides (fragment)
C/Species: Rhodobacter sphaeroides
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C/Accession: C40638
R/Rott, M.A.; Wittuhn, V.C.; Schilke, B.A.; Soranno, M.; All, A.; Donohue, T.J.
J. Bacteriol. 175, 358-366, 1993
A/Title: Genetic evidence for the role of isocytochrome c2 in photosynthetic growth of R

A/Reference number: A40638; MUID:93123153; PMID:8380401
A/Accession: C40638
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-29 <ROR>
A/Note: sequence extracted from NCBI backbone (NCBI:122345, NCBI:123661)

Query Match 30.5%; Score 37.5; DB 2; Length 29;
Best Local Similarity 41.7%; Pred. No. 68;
Matches 10; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

QY 2 RGRSPSWGPDPHRSRV 20
DB 5 QGFRPRHGAIGDRHTLGLKDRSV 28

RESULT 3
B70566

Probable ribosomal protein l36 - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C/Accession: B70566
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MIMD:9829587; PMID:9634230
A/Accession: B70566
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A/Residues: 1-37 <COL>
A/Cross-references: GB:295390; GB:AL123456; NID:G3261766; PIDN:CAB08727.1; PID:G2104384
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: rpmJ
C/Superfamily: Escherichia coli ribosomal protein l36

Query Match 27.6%; Score 34; DB 2; Length 37;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18
DB 28 SPDRKOR 35

RESULT 4

S43011
mead protein - Yersinia enterocolitica transposon TN3926 (fragment)

C/Species: Yersinia enterocolitica
C/Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 08-Oct-1999
C/Accession: S43011
R/Osbourn, S.E.V.; Turner, A.K.; Grinstead, J.
Submitted to the EMBL Data Library, March 1994
A/Description: The structure of the bacterial transposable element, TN3926.
A/Reference number: S43011
A/Accession: S43011
A/Molecule type: DNA
A/Residues: 1-24 <OSB>
A/Cross-references: EMBL:X78059; NID:G460067; PIDN:CA54977.1; PID:G460068
C/Genetics:
A/Gene: mead
A/Mobile element: transposon TN3926

Query Match 27.2%; Score 33.5; DB 2; Length 24;
Best Local Similarity 43.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 2 RGRSPWGPDP-RHR 16
DB 3 RPSKCMWPCQPNRHK 18

RESULT 5

S51593
myrB protein - Micromonospora griseorubida (fragment)

C/Species: Micromonospora griseorubida
C/Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C/Accession: S51593
R/Inouye, M.; Takada, Y.; Muto, N.; Beppu, T.; Horinouchi, S.
Mol. Gen. Genet. 245, 456-464, 1994
A/Title: Characterization and expression of a P-450-like mycinamicin biosynthesis gene u
A/Reference number: S51593; MIMD:95107242; PMID:7808395
A/Accession: S51593
A/Molecule type: DNA
A/Residues: 1-28 <INO>
A/Cross-references: EMBL:D16098; NID:G286050; PIDN:BA03671.1; PID:d1004186; PID:G829046
C/Genetics:
A/Gene: myrB

Query Match 26.8%; Score 33; DB 2; Length 28;
Best Local Similarity 52.4%; Pred. No. 2.8e+02;
Matches 11; Conservative 0; Mismatches 6; Indels 4; Gaps 2;

QY 1 PRGRSPWGPDPHRSRNVG 21
DB 11 PRGRS--GP--PRARRGG 27

RESULT 6

IRTRIA
protamine 1A - rainbow trout

N/Alternate names: iridine
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
C/Accession: A02670
R/Ando, T.; Watanabe, S.
Int. J. Protein Res. 1, 221-224, 1969
A/Title: A new method for fractionation of protamines and the amino acid sequences of sa
A/Reference number: A91774; MIMD:72030546; PMID:4553052
A/Accession: A02670
A/Molecule type: protein
A/Residues: 1-33 <AND>
C/Superfamily: protamine Y2
C/Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 26.8%; Score 33; DB 1; Length 33;
Best Local Similarity 45.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 PRGRSPWGPDPHRSRNV 20
DB 1 PRRRSSRPVRRRRRRRV 20

RESULT 7

DB7154
50S ribosomal protein l36 [imported] - Mycobacterium leprae

C/Species: Mycobacterium leprae
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-May-2002
C/Accession: DB7154
R/Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd, S.; Davies, R.M.; Devlin, K.; Duthey, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MIMD:21128732; PMID:11234002
A/Accession: DB7154
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-37 <STO>
A/Cross-references: GB:AL450380; NID:G13093616; PIDN:CAC30916.1; GSPDB:GN00147
C/Genetics:
A/Gene: rpmJ
C/Superfamily: Escherichia coli ribosomal protein l36

Query Match 26.8%; Score 33; DB 2; Length 37;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 DPRHRSR 18
DB 29 DPRHRSR 35

RESULT 8

T34643
hypothetical protein SC10H5.05 SC10H5.05 - Streptomyces coelicolor

C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C/Accession: T34643

A:Stratus: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-58 <Mat>
A:Cross-references: EMBL:X865563, NID:G902200, PIDD:CA60335.1, PID:G902270
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

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OM protein - protein search, using sw model

Run on: June 29, 2004, 11:58:39 ; Search time 9.47059 Seconds

(without alignment)
115.460 Million cell updates/sec

Title: US-09-509-449C-5
Perfect score: 123
Sequence: 1 PRGSRPMSW3PTDPRHSRNVG 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 3234

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	30.1	38	1	RL36_STRPY
2	34	27.6	37	1	RL36_MYCTU
3	34	27.6	38	1	RL36_RASO
4	33	26.8	38	1	PR12_ONCMY
5	33	26.8	37	1	RL36_MYCLE
6	32	26.0	38	1	RL36_LACIA
7	31	25.2	32	1	PR17_ONCMY
8	31	25.2	32	1	PR17_ONCMY
9	31	25.2	37	1	RL36_HAEN
10	31	25.2	37	1	RL36_PASMU
11	30.5	24.8	38	1	FER_METPR
12	30	24.4	32	1	NEUB_PIG
13	30	24.4	37	1	RL36_LBFIN
14	30	24.4	37	1	RL36_SYEL
15	30	24.4	38	1	RL36_BUCAL
16	30	24.4	38	1	RL36_BUCAP
17	30	24.4	40	1	MPAL_USRMA
18	29	23.6	32	1	CH12_STROT
19	29	23.6	32	1	PRT1_ONCKE
20	29	23.6	32	1	PRT5_ONCMY
21	29	23.6	32	1	PRT6_ONCMY
22	29	23.6	32	1	PRT9_ONCMY
23	29	23.6	34	1	THEM_MALSU
24	29	23.6	37	1	RK36_ARATH
25	29	23.6	37	1	RK36_EPRVI
26	29	23.6	37	1	RK36_LOTUA
27	29	23.6	37	1	RK36_OSNHO
28	29	23.6	38	1	RL36_PSEAB
29	29	23.6	38	1	RL36_PSEPK
30	29	23.6	39	1	ABAE_BOMPA
31	28	22.8	14	1	TAT_HV1W2
32	28	22.8	14	1	TAT_HV1Z8
33	28	22.8	20	1	VMO2_CHICK

34	28	22.8	29	1	RL15_HALCU	P05971 halobacteri
35	28	22.8	34	1	PRT_DICLA	Q9527 dicentrarch
36	28	22.8	37	1	RL36_BIFLO	Q89326 bifidobacte
37	28	22.8	37	1	RL36_NEIMA	Q9152 neisseria m
38	28	22.8	37	1	RL36_STRCO	Q86772 streptomyce
39	27	22.0	27	1	PR1B_ACIQU	P02323 acipenser g
40	27	22.0	28	1	PAC2_PSEPO	P20360 pseudochis
41	27	22.0	30	1	AATW_RABIT	P12345 oryctolagus
42	27	22.0	33	1	PR1B_MUGCE	P08130 mugil cepha
43	27	22.0	34	1	PRT1_SAROR	P25127 sarda orien
44	27	22.0	34	1	PRT1_SCOSC	P83264 scomber sco
45	27	22.0	34	1	PRT2_THUTH	P02322 thunnus thy

ALIGNMENTS

RESULT 1	ID	RL36_STRPY	STANDARD;	PRT;	38 AA.
AC	Q9A1V2				
DT	28-FEB-2003 (rel. 41, Created)				
DT	28-FEB-2003 (rel. 41, Last sequence update)				
DT	15-MAR-2004 (rel. 43, Last annotation update)				
DE	50S ribosomal protein L36.				
GN	RPMU OR SPY0076 OR SPYM3_0063 OR SPS0065 OR SPYWL8_0076 OR GBS0081 OR SAG0081 OR SMU.2003A.				
OS	Streptococcus pyogenes, (serotype M3)				
OS	Streptococcus pyogenes, (serotype M18)				
OS	Streptococcus agalactiae (serotype IIT)				
OS	Streptococcus agalactiae (serotype V), and				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_TaxID=1314, 198466, 186103, 216495, 216466, 1309;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=S.pyogenes; STRAIN=SF370 / ATCC 700294 / Serotype M1;				
RX	MEDLINE=21192684; PubMed=11296296;				
RA	Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Via H.G., Najat F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;				
RA	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";				
RA	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;				
RX	MEDLINE=22133808; PubMed=1212206;				
RA	Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Perkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.;				
RA	"Genome sequence of a serotype M3 strain of group A Streptococcus: phase-encoded toxins, the high-virulence phenotype, and clone emergence.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;				
RX	MEDLINE=2268378; PubMed=12799345;				
RA	Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y., Okazaki N., Kawabata S., Yamazaki K., Shida T., Yasunaga T., Hayashi H., Hattori M., Hamada S.;				
RA	"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution.";				
RT	Genome Res. 13:1042-1055(2003).				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=S.pyogenes; STRAIN=MGAS832 / Serotype M18;				
RX	MEDLINE=21927593; PubMed=11917108;				

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CC -----
DR EMBL; Z95390; CAB08727.1; -
DR EMBL; AE007160; AAK47907.1; -
DR EMBL; U15140; AAB17596.1; -
DR EMBL; BX248346; CAD95677.1; -
DR PIR; B70566; B70566.
DR HSP; P80256; 1DPE.
DR TIGR; MT3567.1; -
DR Tubercula; RV3461c; -
DR HAVAP; MF_00251; -; 1.
DR InterPro; IPR000473; Ribosomal_L36.
DR Pfam; PF00444; Ribosomal_L36; 1.
DR ProDom; PD002101; Ribosomal_L36; 1.
DR TIGRFAMs; TIGR01022; rpm1_bact; 1.
DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
KW Ribosomal protein, Complete proteome.
SQ SEQUENCE 37 AA; 4343 MW; C92A4845315F930F CRC64;

Query Match 27.6%; Score 34; DB 1; Length 37;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18
DB 28 SDRHQR 35

RESULT 3
ID R136_RALSO STANDARD; PRT; 38 AA.

AC Q8XV34;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 50S ribosomal protein L36.
GN RPM1 OR RSC2997 OR RSO1115.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OX Burkholderiaceae; Ralstonia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cartolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Signer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RT Genome sequence of the plant pathogen Ralstonia solanacearum;
RL Nature 415:497-502 (2002).
CC -1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.

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CC -----
DR EMBL; AL646073; CAD16706.1; -
DR HAVAP; MF_00251; -; 1.
DR InterPro; IPR000473; Ribosomal_L36.
DR Pfam; PF00444; Ribosomal_L36; 1.
DR ProDom; PD002101; Ribosomal_L36; 1.
DR TIGRFAMs; TIGR01022; rpm1_bact; 1.

DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
KW Ribosomal protein, Complete proteome.
SQ SEQUENCE 38 AA; 4392 MW; 29FB9F24F106545 CRC64;

Query Match 27.6%; Score 34; DB 1; Length 38;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18
DB 29 SDRHQR 36

RESULT 4
ID PR12_ONCMY STANDARD; PRT; 33 AA.

AC P02328;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Protamine 1A (Iridine 1A).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=72030546; PubMed=4953052;
RA Ando T., Watanabe S.;
RT "A new method for fractionation of protamines and the amino acid
RT sequences of salmon and three components of iridine";
RL Int. J. Protein Res. 1:221-224 (1969).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
DR PIR; A02670; IRTRIA.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 33 AA; 4406 MW; F82C0A9C080A1FFP2 CRC64;

Query Match 26.8%; Score 33; DB 1; Length 33;
Best Local Similarity 45.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 PRGSRPVGWPTDPRHRSRV 20
DB 1 PRRRSSRPVRRRRRRRV 20

RESULT 5
ID R136_MYCLE STANDARD; PRT; 37 AA.

AC Q9X7A2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L36.
GN RPM1 OR ML1961 OR MLCB1222.31C.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Sigleweiler K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier C., Harris D.,
RA Mungall K., Baaham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Randalstead M.A., Ruthertford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.
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 CC -----
 CC EMBL: A1049491; CAB39837.1; -;
 CC EMBL: A1583923; CAC30916.1; -;
 CC FIR: D87154; D87154.
 CC HSSP: P80256; IDFE.
 CC DR Leptoma; ML1961; -;
 CC DR HAMAP; MF_00251; -;
 CC DR InterPro; IPR000473; Ribosomal_L36.
 CC DR Pfam; PF00444; Ribosomal_L36; 1.
 CC DR TIGRFA; TIGR01022; rpm1_bact; 1.
 CC DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
 CC KW Ribosomal protein; Complete proteome.
 CC SQ SEQUENCE 37 AA; 4458 MW; D22FA941710B496F CRC64;
 CY 12 DPRHRSR 18
 DB 29 DPKHRSR 35
 Query Match 26.8%; Score 33; DB 1; Length 37;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
 ID L36 LACIA STANDARD; PRT; 38 AA.
 AC P27146;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L36.
 GN Rpm1 OR L36271 OR SPO233 OR SPO232.
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris),
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris),
 OS Streptococcus pneumoniae, and
 OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360, 1359, 1313, 171101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.l.cremoris; STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Mincker P., Mauger S., Jallion O., Malarme K.,
 RA Weissenbach U., Shilich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.l.cremoris; STRAIN=MG1614;
 RX MEDLINE=92148378; PubMed=1783905;
 RA Koyula T., Hemila H.;
 RT "Nucleotide sequence of a Lactococcus lactis gene cluster encoding
 RT adenylate kinase, initiation factor 1 and ribosomal proteins.";
 RL J. Gen. Microbiol. 137:2595-2600(1991).
 RN [3]
 RP SEQUENCE FROM N.A.

RC SPECIES=L.l.cremoris; STRAIN=MG1614;
 RX MEDLINE=91348245; PubMed=1908794;
 RA Koyula T., Palva I., Hemila H.;
 RT "Nucleotide sequence of the secY gene from Lactococcus lactis and
 RT identification of conserved regions by comparison of four secY
 RT proteins.";
 RL FEMS Lett. 288:114-118(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.pneumoniae; STRAIN=ATCC BAA-255 / TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tedell H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolony J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Ulfbeck T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Anguilo S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.pneumoniae; STRAIN=ATCC BAA-255 / R6;
 RX MEDLINE=2428245; PubMed=11544234;
 RA Hoskins U., Aldorn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 RA Dehoff B.S., Estrem S.T., Filtz L., Fu D.-J., Fuller W., Geringer C.,
 RA Gilmour R., Glas J.S., Khoja H., Kraft A.R., Lagace R.E.,
 RA Lebman D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 RA McAlaren S.M., McHenry M., McLeaster K., Mundy C.W., Nicas T.I.,
 RA Norris F.H., O'Garra M., Peery R.B., Robertson G.T., Rokey P.,
 RA Sun P.-W., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Scharnd P.L.,
 RA Glas J.L.;
 RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
 RL J. Bacteriol. 183:5709-5717(2001).
 CC -1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.
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 CC EMBL: AE006436; AAK06169.1; -;
 CC EMBL: X59250; CAA1942.1; -;
 CC EMBL: AE007336; AAK74413.1; -;
 CC EMBL: AE008402; AAK99016.1; -;
 CC DR PIR; D95027; D95027.
 CC DR PIR; D97898; D97898.
 CC DR PIR; S17899; S17899.
 CC DR HSSP; P80256; IDFE.
 CC DR TIGR; SPO233; -;
 CC DR HAMAP; MF_00251; -;
 CC DR InterPro; IPR000473; Ribosomal_L36.
 CC DR Pfam; PF00444; Ribosomal_L36; 1.
 CC DR ProDom; PD002101; Ribosomal_L36; 1.
 CC DR TIGRFA; TIGR01022; rpm1_bact; 1.
 CC DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
 CC KW Ribosomal protein; Complete proteome.
 CC SQ SEQUENCE 38 AA; 4421 MW; 892FEFE9A5939D88 CRC64;
 CY 10 PTPDPRHRSR 18
 DB 28 DPKHRSR 36
 Query Match 26.8%; Score 32; DB 1; Length 38;
 Best Local Similarity 44.4%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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RESULT 7
PRT1 ONCMY STANDARD; PRT; 32 AA.
AC P08146;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine TP16.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procatanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_Taxid=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83272939; PubMed=6308564;
RA Aiken J.N., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;
RT "Sequence homologues in the protamine gene family of rainbow trout.";
RL Nucleic Acids Res. 11:4907-4922(1983).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
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DR EMBL; X01597; CAA25750.1; -
DR PIR; C21211; C21211.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET
SQ SEQUENCE 32 AA; 4323 MW; B07A9C9D8CC796FF CRC64;

Query Match 25.2%; Score 31; DB 1; Length 32;
Best Local Similarity 44.4%; Pred. No. 2.5e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPDPHRSR 18
DB 1 FRRRSSRPVRRRRAR 18

RESULT 8
PRT8 ONCMY STANDARD; PRT; 32 AA.
AC P12817;
DT 01-OCT-1988 (Rel. 12, Created)
DT 01-OCT-1988 (Rel. 12, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Protamine 2A.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procatanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_Taxid=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=86274711; PubMed=3155398;
RA McKay D.J., Renaux B.S., Dixon G.H.;
RT "Rainbow trout protamines. Amino acid sequences of six distinct
RT proteins from a single testis.";
RL Eur. J. Biochem. 158:361-366(1986).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive complex.

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CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- TISSUE SPECIFICITY: Testis.
-----
DR PIR; E21211; E21211.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 32 AA; 4224 MW; B07A9C9D90B796FF CRC64;

Query Match 25.2%; Score 31; DB 1; Length 32;
Best Local Similarity 44.4%; Pred. No. 2.5e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 PRGSRPSWGPDPHRSR 18
DB 1 FRRRSSRPVRRRRAR 18

RESULT 9
PRT6 HAETN STANDARD; PRT; 37 AA.
AC P46361;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L36.
GN RPL36 OR RPL36 OR H10798.1.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_Taxid=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams W.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips R.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utecherback T.R., Hanna M.C., Spriggs T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.
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DR EMBL; U32762; AAC22457.1; -
DR HSSP; P80256; IDPE.
DR TIGR; H10798.1; -
DR HAMAP; MF_00251; -
DR InterPro; IPR000473; Ribosomal L36.
DR Pfam; PF00444; Ribosomal L36; 1.
DR ProDom; PD002101; Ribosomal L36; 1.
DR TIGRFAMs; TIGR01022; rplL36; 1.
DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 37 AA; 4297 MW; 53AE5B5D828F83D CRC64;

Query Match 25.2%; Score 31; DB 1; Length 37;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18

```

Db 28 SDPKKOR 35

RESULT 10

ID RL36_PASMU STANDARD; PRT; 37 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 50S ribosomal protein L36.

GN RPL36 OR RPL36 OR PM1394.

OS Pasteurella multocida.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Pasteurella.

OC NCBI_TaxID=7477;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Pm70;

RX MEDLINE=21145866; PubMed=11248100;

RA May B.U., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;

RT "Complete genomic sequence of Pasteurella multocida Pm70.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

CC -1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.

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DR EMBL; AE006177; AK03478.1; -

DR HSSP; P80256; 1DEF.

DR HAMAP; MF_00251; -; 1.

DR InterPro; IPR000473; Ribosomal_L36.

DR Pfam; PF00444; Ribosomal_L36; 1.

DR ProDom; PD002101; Ribosomal_L36; 1.

DR TIGRfam; TIGR01022; rplL_bact; 1.

DR PROSITE; PS00628; RIBOSOMAL_L36; 1.

KM Ribosomal protein; Complete proteome.

SQ SEQUENCE 37 AA; 4279 MW; 53A85B4CB39F83D CRC64;

Query Match 25.2%; Score 31; DB 1; Length 37;

Best Local Similarity 50.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18

Db 28 SDPKKOR 35

RESULT 11

ID_FER_METPR STANDARD; PRT; 38 AA.

AC P81542;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Zinc-containing ferredoxin (Seven-iron ferredoxin) (Fragment).

GN ZFX.

OS Metallophthora prunae.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

OC Metallophthora.

OC NCBI_TaxID=47304;

OK (1)

RP SEQUENCE.

RA Gomes C.M., Faria A., Carita J., Mendes J.C., Regalia M., Chicau P.,

RA Huber H., Stetter K.O., Teixeira M.;

RT "Di-cluster, seven iron ferredoxins from hyperthermophilic

RT Sulfolobales.";

RL J. Biol. Inorg. Chem. 3:499-507(1998).

CC -1- FUNCTION: Ferredoxins are iron-sulfur proteins that transfer

CC electrons in a wide variety of metabolic reactions.

CC -1- COFACTOR: Binds one 3Fe-4S and one 4Fe-4S cluster and one zinc

CC atom (By similarity).

CC -1- SIMILARITY: Belongs to the bacterial-type ferredoxin family.

DR HSSP; P55907; 1YXR.

KM Electron transport; Iron-sulfur; Repeat; 4Fe-4S; 3Fe-4S; Methylation;

Zinc.

FT DOMAIN 1 38 N-TERMINAL EXTENSION.

FT METAL 16 16 ZINC.

FT METAL 19 19 ZINC.

FT METAL 37 37 ZINC.

FT MOD RES 30 30 METHYLATION.

FT NON TER 38 38

SQ SEQUENCE 38 AA; 4006 MW; 256D378618BC9ED5 CRC64;

Query Match 24.8%; Score 30.5; DB 1; Length 38;

Best Local Similarity 31.0%; Pred. No. 3.5e+02;

Matches 9; Conservative 3; Mismatches 8; Indels 9; Gaps 1;

QY 2 RGRPSWG-----PTDPRHRSRVG 21

Db 7 RTRRPVTDGAGKRVNAPDPVYKXALG 35

RESULT 12

ID_NEUB_PIG STANDARD; PRT; 32 AA.

AC P01297;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuromedin B-32 [Contains: Neuromedin B].

GN NMB.

OS Sus scrofa (pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=99823;

RP SEQUENCE.

RX MEDLINE=85279454; PubMed=4026853;

RA Minamino N., Stroh T., Kangawa K., Matsuo H.;

RT "Neuromedin B-32 and B-30: two 'big' neuromedin B identified in

RT porcine brain and spinal cord.";

RL Biochem. Biophys. Res. Commun. 130:685-691(1985).

RN [2]

RP SEQUENCE.

RA Minamino N., Kangawa K., Matsuo H.;

RT "Neuromedin B and neuromedin C: two mammalian bombesin-like peptides

RT identified in pig spinal cord and brain.";

RL Regul. Pept. 19:127-127(1987).

[3]

SEQUENCE OF 23-32.

RX MEDLINE=83282813; PubMed=6882442;

RA Minamino N., Kangawa K., Matsuo H.;

RT "Neuromedin B: a novel bombesin-like peptide identified in porcine

RT spinal cord.";

RL Biochem. Biophys. Res. Commun. 114:541-548(1983).

CC -1- FUNCTION: Stimulates smooth muscle contraction in a manner similar

CC to that of bombesin.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the bombesin/neuromedin B/zanarensin

CC family.

DR PIR; B60301; BSRGN.

DR InterPro; IPR000874; Bombesin.

DR Pfam; PFO2044; Bombesin; 1.

DR PROSITE; PS00257; BOMBESIN; 1.

KM Bombesin family; Amidation.

FT PEPTIDE 23 32 NEUROMEDIN B.

FT MOD RES 32 32 AMIDATION.

SQ SEQUENCE 32 AA; 3654 MW; 7B3FC92C953D80 CRC64;

Query Match 24.4%; Score 30; DB 1; Length 32;

Best Local Similarity 35.7%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 SWGPTDPRHSRNV 20
Db 4 SWDPEPRSRAGK 17

RESULT 13

RL36 LEPIN

ID

RL36 LEPIN

STANDARD; PRT; 37 AA.

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 50S ribosomal protein L36.

GN RPL36 OR LA0761.1.

OS Leptospira interrogans.

OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.

NCBI_TaxID=173;

[1]

SEQUENCE FROM N.A.

RC STRAIN=Iai / Serogroup Icterohaemorrhagiae / Serovar Iai;

RX MEDLINE=20088935; PubMed=10620683;

RA Zuercher R.L., Hartkeerl R.A., van de Kemp H., Bal A.E.;

RT "Characterization of the Leptospira interrogans S10-spc-alpha

operation".

RL FEMS Microbiol. Lett. 182:303-308 (2000).

[2]

SEQUENCE FROM N.A.

RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar Iai;

RX MEDLINE=2258143; PubMed=12712204;

RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Jiang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Sheng H.-H., Yin H.-F.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi W.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;

RT Unique physiological and pathogenic features of Leptospira

interrogans revealed by whole-genome sequencing.";

RL Nature 422:888-893 (2003).

-1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.

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RESULT 14

RL36 SYNEL

ID

RL36 SYNEL

STANDARD; PRT; 37 AA.

AC 08DMT2;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE 50S ribosomal protein L36.

GN RPL36 OR TSP0102.

OS Synecococcus elongatus (Thermosynechococcus elongatus).

OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.

NCBI_TaxID=32046;

[1]

SEQUENCE FROM N.A.

RC STRAIN=BP-1;

RX MEDLINE=2225144; PubMed=12240834;

RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,

Watanabe A., Iriuchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Nakazaki N.,

Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the thermophilic cyanobacterium

Thermosynechococcus elongatus BP-1.";

RL DNA Res. 9:123-130 (2002).

-1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.

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RT Buchnera sp. APS."
RL Nature 407:81-86(2000).
CC -1- SIMILARITY: Belongs to the L36P family of ribosomal proteins.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP001119; BAB13196.1; -.
DR HSSP; P80256; 1DPE.
DR HAMAP; MF_00251; -; 1.
DR InterPro; IPR000473; Ribosomal_L36.
DR Pfam; PF00444; Ribosomal_L36; 1.
DR ProDom; PD002101; Ribosomal_L36; 1.
DR TIGRFAMs; TIGR01022; rpmu_dact; 1.
DR PROSITE; PS00828; RIBOSOMAL_L36; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 38 AA; 4365 MW; 29F271414AA25621 CRC64;

```

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Query March 24.4%; Score 30; DB 1; Length 38;
Best Local Similarity 57.1%; Pred. No 4,1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 12 DRRHRSR 18
Db 30 DPKHKQR 36

```

Search completed: June 29, 2004, 12:06:32
 Job time : 10.4706 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2004, 12:01:59 ; Search time 38.2941 Seconds
(without alignments)
173.026 Million cell updates/sec

Title: US-09-509-449C-5
Perfect score: 123
Sequence: 1 PRGSRPWSGPTDPRHRSRVNG 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 31556

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.5	32.9	39	2	Q9X689 mercury res
2	39.5	32.1	33	6	Q77492 nycticebus
3	38	30.9	21	11	Q922Y9 mus musculus
4	38	30.9	23	12	Q66184 porcine res
5	38	30.9	23	12	Q66204 transmissib
6	38	30.9	37	16	Q7WR41 bordetella
7	38	30.9	37	16	Q7W2D3 bordetella
8	38	30.9	37	16	Q7VTA8 bordetella
9	38	30.9	40	15	Q9YP98 icos sarcom
10	37.5	30.5	29	2	Q05846 rhododact
11	36	29.3	27	5	Q95WF4 acropora mi
12	36	29.3	39	12	Q66546 human herpe
13	35	28.5	34	5	Q819U9 periplaneta
14	35	28.5	37	16	Q7WKF4 haemophilus
15	34.5	28.0	22	4	O95597 homo sapien
16	34.5	28.0	35	13	Q801Y0 carassius a

17	33.5	27.2	24	2	Q56907	Q56907 yersinia en
18	33	26.8	20	13	Q42534	Q42534 brachydanio
19	33	26.8	29	15	Q91QJ4	Q91QJ4 human immun
20	33	26.8	29	15	Q91QJ2	Q91QJ2 human immun
21	33	26.8	29	15	Q91QJ6	Q91QJ6 human immun
22	33	26.8	29	15	Q91QJ3	Q91QJ3 human immun
23	33	26.8	35	16	Q7UTU8	Q7UTU8 rhodospirell
24	33	26.8	38	16	Q7UTU5	Q7UTU5 rhodospirell
25	33	26.8	40	2	Q9R4G1	Q9R4G1 bacillus sp
26	32.5	26.4	29	16	Q86497	Q86497 streptomyce
27	32	26.0	25	5	Q18630	Q18630 sphaerectin
28	32	26.0	26	12	Q56480	Q56480 hepatitis c
29	32	26.0	26	12	Q56481	Q56481 hepatitis c
30	32	26.0	28	13	Q42517	Q42517 myxine glut
31	32	26.0	29	15	Q91QJ4	Q91QJ4 human immun
32	32	26.0	29	15	Q91QJ7	Q91QJ7 human immun
33	32	26.0	29	15	Q91QJ5	Q91QJ5 human immun
34	32	26.0	29	15	Q91QJ6	Q91QJ6 human immun
35	32	26.0	38	8	Q33303	Q33303 zea mays (m
36	32	26.0	38	15	Q88384	Q88384 simian t-ly
37	32	26.0	39	16	Q83921	Q83921 enterococcu
38	32	26.0	39	4	Q9UB06	Q9UB06 homo sapien
39	32	26.0	39	5	Q18620	Q18620 blomphalaxi
40	32	26.0	39	16	Q7UTU9	Q7UTU9 rhodospirell
41	32	26.0	39	16	Q7UTU5	Q7UTU5 rhodospirell
42	31.5	25.6	36	16	Q7UG44	Q7UG44 rhodospirell
43	31	25.2	17	12	Q66202	Q66202 transmissib
44	31	25.2	12	12	Q85004	Q85004 porcine res
45	31	25.2	27	4	Q9UM46	Q9UM46 homo sapien

ALIGNMENTS

RESULT 1	Q9X689	PRELIMINARY;	PRT;	39 AA.
ID	Q9X689			
AC	Q9X689;			
DT	01-NOV-1999 (TREMBlrel. 12, Created)			
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)			
DT	01-NOV-1999 (TREMBlrel. 12, Last annotation update)			
DE	Merd (Fragment).			
GN	MERD.			
OS	mercury resistant bacterium '96 SE13.			
OC	Bacteria.			
OX	NCBI_TaxID=93601;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=96 SE13.			
RA	Holt R.J., Bruce K.D., Strike P.;			
RT	"Conservation of transposon structures in soil bacteria.";			
RL	FEMS Microbiol. Ecol. 0:0-0(1999).			
DR	EMBL; AF134211; AAD34398.1; -.			
FT	NON TER			
SEQ	SEQUENCE 39 AA, 4421 MW, 9A35BCDFOF5D258 CRG64;			
Query Match	32.9%; Score 40.5; DB 2; Length 39;			
Best Local Similarity	40.0%; Pred. No. 77;			
Matches	10; Conservative 3; Mismatches 5; Indels 7; Gaps 2;			
QY	3 GSRP-----SWGPTDP-RHRSRV 20			
DB	5 GARPWPAKCKWPPCQPNRHSIRV 29			
RESULT 2	Q77492	PRELIMINARY;	PRT;	33 AA.
ID	Q77492			
AC	Q77492;			
DT	01-NOV-1998 (TREMBlrel. 08, Created)			
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)			
DT	01-NOV-2003 (TREMBlrel. 24, Last annotation update)			
DE	D4 dopamine receptor (D4DR) (Fragment).			

OS Nycticebus coucang (Slow loris).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Strepsithini; Loridae; Nycticebus.
 OX NCBI_TaxID=9470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Inoue-Murayama M., Takenaka O., Murayama Y.,
 RT "Origin and divergence of tandem repeats of primate D4 dopamine
 receptor genes.";
 RL Primates 39:217-224(1998).
 DR EMBL: AB016201; BAA32039.1; -;
 DR GO: GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON TER 1
 FT NON TER 33
 SQ SEQUENCE 33 AA; 3541 MW; 4AF17501A4FD5CEC CRC64;

Query Match 32.1%; Score 39.5; DB 6; Length 33;
 Best Local Similarity 54.5%; Pred. No. 91;
 Matches 12; Conservative 1; Mismatches 4; Indels 5; Gaps 2;

QY 1 RGSRPSPGPTDPRH---RSR 18
 DB 1 PR-SRPAPGPPRRRLGPRSR 21

RESULT 3
 ID Q922Y9 PRELIMINARY; PRT; 21 AA.
 AC Q922Y9;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC006692; AAH06692.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 21 AA; 2315 MW; 60698D703D0C1692 CRC64;

Query Match 30.9%; Score 38; DB 11; Length 21;
 Best Local Similarity 75.0%; Pred. NO. 94;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RGSRPSPW 8
 DB 14 PRGSSPCW 21

RESULT 4
 ID Q66184 PRELIMINARY; PRT; 23 AA.
 AC Q66184;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Coronavirus PRCV nucleoprotein, 5' region (fragment).
 OS Porcine respiratory coronavirus.
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 CC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11146;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=PRCV 86/137004 (British Isolate);
 RC Page K.W., Britton P., Boursnell M.E.G.;
 RT "Sequence analysis of the leader RNA of two porcine coronaviruses:
 transmissible gastroenteritis virus and porcine respiratory

RT coronavirus";
 RL Virus Genes 0:0-0(1990).
 DR EMBL: X52668; CA36895.1; -;
 DR PIR: S10448; S10448.
 DR GO: GO:0019013; C:viral nucleocapsid; IEA.
 KW Nucleocapsid.
 FT NON TER 23
 SQ SEQUENCE 23 AA; 2565 MW; D761FC279767540F CRC64;

Query Match 30.9%; Score 38; DB 12; Length 23;
 Best Local Similarity 38.9%; Pred. NO. 1e+02;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 RGSRPSPGPTDPRHSRN 19
 DB 4 QGQRVSGDSESTKIRGRS 21

RESULT 5
 ID Q66204 PRELIMINARY; PRT; 23 AA.
 AC Q66204;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Coronavirus TGEV nucleoprotein, 5' region (fragment).
 OS Transmissible gastroenteritis virus.
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 CC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=TGEV F572/70 (Virulent British Isolate);
 RC Page K.W., Britton P., Boursnell M.E.G.;
 RT "Sequence analysis of the leader RNA of two porcine coronaviruses:
 transmissible gastroenteritis virus and porcine respiratory
 coronavirus";
 RL Virus Genes 0:0-0(1990).
 DR EMBL: X52157; CA36410.1; -;
 DR PIR: S10448; S10448.
 DR GO: GO:0019013; C:viral nucleocapsid; IEA.
 KW Nucleocapsid.
 FT NON TER 23
 SQ SEQUENCE 23 AA; 2565 MW; D761FC279767540F CRC64;

Query Match 30.9%; Score 38; DB 12; Length 23;
 Best Local Similarity 38.9%; Pred. NO. 1e+02;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 RGSRPSPGPTDPRHSRN 19
 DB 4 QGQRVSGDSESTKIRGRS 21

RESULT 6
 ID Q7MRAL PRELIMINARY; PRT; 37 AA.
 AC Q7MRAL;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE 50S ribosomal protein 136.
 GN RPM2 OR B80053.
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=RB50 / ATCC BAA-588;
 RX MEDLINE=22827554; PubMed=12910271;
 RA Patricki U., Sebatina M., Preston A., Murphy L.D., Thomson N.,
 Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrrell B.G., Maskell D.J.,
 RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
 RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640437; CAB30555.1;
 KM Ribosomal protein; Complete proteome.
 SQ SEQUENCE 37 AA; 4332 MW; 53B3BBE5487DADD CRC64;

Query Match 30.9%; Score 38; DB 16; Length 37;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18
 DB 28 TDPHRSR 35

RESULT 7
 Q7WZD3 PRELIMINARY; PRT; 37 AA.
 AC Q7WZD3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 50S ribosomal protein 136.
 GN RPMJ OR BP0053.
 OS *Bordetella parapertussis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=12822 / ATCC BAA-587;
 RX MEDLINE=22827954; PubMed=12910271;

RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrrell B.G., Maskell D.J.,
 RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
 RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640423; CAB39794.1;
 KM Ribosomal protein; Complete proteome.
 SQ SEQUENCE 37 AA; 4332 MW; 53B3BBE5487DADD CRC64;

Query Match 30.9%; Score 38; DB 16; Length 37;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18
 DB 28 TDPHRSR 35

RESULT 8
 Q7VTA9 PRELIMINARY; PRT; 37 AA.
 AC Q7VTA9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 50S ribosomal protein 136.
 GN RPMJ OR BP3638.
 OS *Bordetella pertussis*.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
 RX MEDLINE=22827954; PubMed=12910271;
 RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.,
 RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
 RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
 RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
 RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
 RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
 RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
 RA Rabinowitsch E., Rutter S., Sanders M., Saunders R., Seeger K.,
 RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
 RA Unwin L., Whitehead S., Barrrell B.G., Maskell D.J.,
 RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
 RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
 RL Nat. Genet. 35:32-40(2003).
 DR EMBL; BX640422; CAB3895.1;
 KM Ribosomal protein; Complete proteome.
 SQ SEQUENCE 37 AA; 4332 MW; 53B3BBE5487DADD CRC64;

Query Match 30.9%; Score 38; DB 16; Length 37;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18
 DB 28 TDPHRSR 35

RESULT 9
 Q9YFG8 PRELIMINARY; PRT; 40 AA.
 AC Q9YFG8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE (Prague "wild type") src gene; amino acids 1-40 (fragment).
 OS Rous sarcoma virus.
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 OC NCBI_TaxID=11886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=831633; PubMed=6304353;
 RA Kitamura N., Yoshida M.,
 RT "Small deletion in src of Rous sarcoma virus modifying transformation
 RT phenotypes: Identification of 207-nucleotide deletion and its smaller
 RT product with protein kinase activity.";
 RL J. Virol. 46:985-992(1983).
 DR EMBL; J02349; AAA42577.1;
 FT NON TER
 SQ SEQUENCE 40 AA; 3989 MW; 11DECBF9FBD3064 CRC64;

Query Match 30.9%; Score 38; DB 15; Length 40;
 Best Local Similarity 53.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 9 GPTDPRHSRNVG 21
 DB 7 GPTDPRHSRNVG 19

RESULT 10
 Q05846 PRELIMINARY; PRT; 29 AA.
 ID Q05846
 AC Q05846;

```

DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Isocytichrome c2 (cycl) (Fragment).
OC Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OK NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RA Rott M.A., Withum V.C., Schilke B.A., Sorzano M., Ali A.,
RA Donohue T.J.;
RT "Genetic evidence for the role of isocytichrome c2 in photosynthetic
RT growth of Rhodobacter sphaeroides.";
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; L02104; AAA61342.1; -.
DR PIR; C40638; C40638.
FT NON TER 29
SQ SEQUENCE 29 AA; 3263 MW; E8461B87691D3278 CRC64;

Query Match 30.5%; Score 37.5; DB 2; Length 29;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

QY 2 RGSRPWGPDPH-----RSRV 20
Db 5 QGFRPRHGATGDRHTLGLKDRSV 28

RESULT 11
Q95WF4 PRELIMINARY; PRT; 27 AA.
ID Q95WF4;
AC Q95WF4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Nuclear receptor ANNR10 (Fragment).
OC Acropora millepora.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Asterozoellina; Acroporidae; Acropora.
OK NCBI_TaxID=45264;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21490824; PubMed=11603940;
RA Grasso L.C., Hayward D.C., Trueman J.W.H., Hardie K.M., Janssens P.A.,
RA Ball E.E.;
RT "The evolution of nuclear receptors: evidence from the coral
RT Acropora.";
RL Mol. Phylogenet. Evol. 21:93-102(2001).
CC -1 SIMILARITY BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
CC -1 SIMILARITY BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AF323690; AAU29203.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR01628; Znf_C4steroid.
DR Pfam; PF01010; Zf-C4; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON TER 1
FT NON TER 27
SQ SEQUENCE 27 AA; 3302 MW; 2E0C29C3A9691CA5 CRC64;

Query Match 29.3%; Score 36; DB 5; Length 27;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PTDPHRRR 18
Db 19 PVDKRRNR 27

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RESULT 12
Q6546 PRELIMINARY; PRT; 39 AA.
ID Q6546;
AC Q6546;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE EBV B95-8 Cl(e) DNA with antigen coding ORF (Fragment).
OS Human herpesvirus 4 (Epstein-Barr virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OK NCBI_TaxID=10376;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88217505; PubMed=2835748;
RA Walls D., Perricaudet M., Gannon F.;
RT "The analysis of EBV proteins which are antigenic in vivo.";
RT Nucleic Acids Res. 16:2859-2872(1988).
DR EMBL; X07530; CAA30405.1; -.
FT NON TER 39
SQ SEQUENCE 39 AA; 4280 MW; 7937120F24AF5774 CRC64;

Query Match 29.3%; Score 36; DB 12; Length 39;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 4; Gaps 1;

QY 1 PRGSRPW---GTPDRR 16
Db 16 PKAGCRSWPASTGPSTPRSR 35

RESULT 13
Q819U9 PRELIMINARY; PRT; 34 AA.
ID Q819U9;
AC Q819U9;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE large conductance calcium activated potassium channel psiO spliceform
DE 1C (Fragment).
GN PSIO.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattellidae; Blattellidae;
OC Blattellidae; Periplaneta.
OK NCBI_TaxID=6978;
RN [1]
RP SEQUENCE FROM N.A.
RA Deret C., Mesutut S., Walther C., Wicher D.;
RT "Cloning and Alternative splicing of a large conductance calcium-
RT activated potassium channel from Periplaneta americana.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452166; AAN76821.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON TER 1
FT NON TER 34
SQ SEQUENCE 34 AA; 3753 MW; AEDA95254993EBBF CRC64;

Query Match 28.5%; Score 35; DB 5; Length 34;
Best Local Similarity 43.8%; Pred. No. 4.2e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 GSRPWPDPHRRR 18
Db 17 GTRPYGGTLKRRR 32

RESULT 14
Q7VKF4 PRELIMINARY; PRT; 37 AA.
ID Q7VKF4;
AC Q7VKF4;

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 50S ribosomal protein L36.
 GN RPMJ2 OR HD1955.
 OS Haemophilus ducreyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=35000HP / ATCC 700724;
 RA Munson R.S., Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
 RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.,
 RT "The complete genome sequence of Haemophilus ducreyi."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017156; AAP96675.1; -
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 37 AA; 4279 MW; 53A83EB09A2F94ED CRC64;

Query Match 28.5%; Score 35; DB 16; Length 37;
 Best Local Similarity 62.5%; Pred. No. 4.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TDPHRSR 18
 |||:|:
 Db 28 TDPKHQR 35

RESULT 15
 ID 095597 PRELIMINARY; PRT; 22 AA.
 AC 095597;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Bcl-2-JH protein (Fragment).
 GN BCL-2-JH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95316863; PubMed=7796416;
 RA Ji W., Qn G.Z., Ye P., Zhang X.Y., Halabi S., Ehrlich M.,
 RT "Frequent detection of bcl-2/JH translocations in human blood and
 RT organ samples by a quantitative polymerase chain reaction assay."
 RL Cancer Res. 55:2876-2882(1995).
 DR EMBL; S78526; AAD14286.1; -
 FT NON TER 1 1
 SQ SEQUENCE 22 AA; 2440 MW; 39988F2A20589300 CRC64;

Query Match 28.0%; Score 34.5; DB 4; Length 22;
 Best Local Similarity 58.3%; Pred. No. 3.2e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 5 RPSMGPTDPRHR 16
 |||:|:
 Db 10 RP-WGQGNRGR 20

Search completed: June 29, 2004, 12:08:20
 Job time : 40.2941 secs

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